



SEQUENCE LIFTING

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HUMAN PROTEINS HAVING SECRETORY SIGNAL
SEQUENCES AND DNAs ENCODING THESE PROTEINS

RECEIVED

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FastSEQ for Windows Version 4.0

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PRT

Homo sapiens

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Met Lys Val Ser Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala

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Ile Asp Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro

20 25 30

Tyr Tyr Ile Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys

35 40 45

Arg Tyr Ile Tyr Thr Asp Gly Lys Cys Asp Asn Pro Ala Val Val His

50 55 60

Asp Asp Asp Met Pro Lys Arg Glu Gly Gln Gln Val Thr Gln Asp Ile

65 70 75

Gly Lys Asp Asp Asp Ile Asn Lys Gln Lys Leu Tyr His Pro Lys Ile

80 85 90

Ile Ile Asp Val Lys Gln Pro Arg Glu Glu Met Gly Ser Gly Val His

95 100 105

Asp Asp Asp Ile Asp Ile Lys Trp Asp Val Leu Gln Pro Gln Leu

110 115 120

Asp Asp Asp Ile Asp Ile Lys Ile Asp Ile Ile Val Asp Thr Gln Asp

125 130 135

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Lys Val Ala Val Phe Leu Ser Val Ala Leu Gly Thr Gly
 10 15
 Asp Asp Pro Glu Asp Gly Gly Lys His Trp Val Val
 20 25
 Tyr Asp Arg Asp Tyr Tyr Asn Tyr Asp His Ser Asp
 30 35
 Asp His Asp Tyr Asp Asp His Asp Asp Asp His Asp
 40 45
 Met Val Met Met Tyr Asp Asp Ile Ala Tyr Ser Ile Asp Asp
 50 55
 Thr Ile Gly Ile Val Ile Asn Arg Pro Asn Gly Thr Asp Val Tyr
 60 65
 Asp Asp Asp Asp Val Thr Asp Ile Asp Val Thr Ile Asp Asp

1. Glu Asp Lys Ser Val Glu Asp His Gln His Phe Thr Tyr Lys Thr Ile Trp Arg
 5 90 95
 2. Lys Lys Lys Ser Tyr Leu Tyr Phe Thr Gln Ile Lys Ala Glu Val
 10 105 110
 3. Asp Gly Ala Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 15 120 125
 4. Asp Lys Ser Asp Val Pro Leu Lys Thr Gln Glu Ile Glu Val Thr
 20 135 140
 5. Thr Ala Val Ala His Arg Pro Gly Ala Ile Lys Ala Glu Leu Ser
 25 150 155 160
 6. Lys Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu
 30 165 170

1. Glu Asp Lys Ser Val Glu Asp His Gln His Phe Thr Tyr Lys Thr Ile Trp Arg
 5 90 95
 2. Lys Lys Lys Ser Tyr Leu Tyr Phe Thr Gln Ile Lys Ala Glu Val
 10 105 110
 3. Asp Gly Ala Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 15 120 125
 4. Asp Lys Ser Asp Val Pro Leu Lys Thr Gln Glu Ile Glu Val Thr
 20 135 140
 5. Thr Ala Val Ala His Arg Pro Gly Ala Ile Lys Ala Glu Leu Ser
 25 150 155 160
 6. Lys Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu
 30 165 170

1. Glu Asp Lys Leu Glu Ile Phe Arg Met Ile Ile Tyr Leu Thr Phe
 5 10 15
 2. Val Ala Met Phe Trp Val Ser Asn Gln Ala Glu Trp Phe Glu Asp
 20 25 30
 3. Asp Val Ile Glu Arg Lys Arg Glu Leu Trp Pro Pro Glu Lys Leu Gln
 35 40 45
 4. Ile Glu Glu Phe Lys Glu Arg Leu Arg Lys Arg Arg Glu Glu Lys
 45 55 60
 5. Lys Arg Asp Ala Gln Gln Asn Ser
 50 70

1. Glu Asp Lys Ser Val Glu Asp His Gln His Phe Thr Tyr Lys Thr Ile Trp Arg
 5 90 95
 2. Lys Lys Lys Ser Tyr Leu Tyr Phe Thr Gln Ile Lys Ala Glu Val
 10 105 110
 3. Asp Gly Ala Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 15 120 125
 4. Asp Lys Ser Asp Val Pro Leu Lys Thr Gln Glu Ile Glu Val Thr
 20 135 140
 5. Thr Ala Val Ala His Arg Pro Gly Ala Ile Lys Ala Glu Leu Ser
 25 150 155 160
 6. Lys Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu
 30 165 170

1. Glu Asp Lys Ser Val Glu Asp His Gln His Phe Thr Tyr Lys Thr Ile Trp Arg
 5 90 95
 2. Lys Lys Lys Ser Tyr Leu Tyr Phe Thr Gln Ile Lys Ala Glu Val
 10 105 110
 3. Asp Gly Ala Ile Glu Tyr Ala Met Ala Tyr Ser Lys Ala Ala Phe
 15 120 125
 4. Asp Lys Ser Asp Val Pro Leu Lys Thr Gln Glu Ile Glu Val Thr
 20 135 140
 5. Thr Ala Val Ala His Arg Pro Gly Ala Ile Lys Ala Glu Leu Ser
 25 150 155 160
 6. Lys Val Ile Val Ala Lys Ala Ser Arg Thr Glu Leu
 30 165 170

Arg Val Arg Asp Val Asp Val Ser Leu Glu Leu Asp Leu Asp Arg
110 115 120 125
Asp Lys Pro Ile Leu Glu Glu Val Met Met Asp Ile Glu Gly Ile Met Ile
130 135 140 145
Asp Arg Met Ile Glu Arg Ser Ile Asp Ile Gly Lys Thr Trp Arg
145 150 155 160
Asp Ile Thr Leu Ala Ala Asp Cys Thr Ser Thr Phe Pro Arg Val
150 155 160 165
Asp Ile Gly Arg Pro Gln Ser Trp Gln Asp Val Arg Cys Gln Ser Leu
165 170 175 180
Asp Ile Asn Pro Asn Ala Arg Leu Asn Gly Gly Lys Val Gln Leu Asn
180 185 190 195
Asp Asp Asp Leu Val Ser Gly Ile Pro Ala Thr Gln Ser Gln Lys Ile
195 200 205 210
Asp Ile Val Gly Glu Ile Thr Asn Leu Arg Val Asn Phe Thr Arg Leu
215 220 225 230
Asp Ile Thr Ile Gln Arg Gly Tyr His Pro Pro Ser Ala Tyr Tyr Ala
230 235 240 245
Thr Asp Gln Leu Arg Leu Gln Gly Ser Cys Phe Cys His Gly His Ala
245 250 255 260
Asp Asp Tyr Ala Pro Lys Pro Gly Ala Ser Ala Gly Pro Ser Thr Ala
260 265 270 275
Thr Glu Val His Asp Val Cys Val Cys Gln His Asn Thr Ala Gly Pro
275 280 285 290
Asp Glu Arg Cys Ala Pro Phe Tyr Asn Asn Arg Pro Trp Arg Pro
295 300 305 310
Asp Glu Gly Gln Asp Ala His Glu Cys Gln Arg Cys Asp Cys Asn Gly
310 315 320 325
His Ile Glu Thr Cys His Phe Asp Pro Ala Val Phe Ala Ala Ser Gln
325 330 335 340
Asp Ala Tyr Gly Gly Val Cys Asp Asn Cys Arg Asp His Thr Glu Gly
340 345 350 355
Asp Asn Ile Glu Arg Cys Gln Leu His Tyr Phe Arg Asn Arg Arg Pro
355 360 365 370
Asp Ala Val Ile Glu Glu Thr Cys Ile Ser Cys Glu Cys Asp Pro Asp
375 380 385 390
Asp Ala Val Pro Gly Ala Pro Cys Asp Pro Val Thr Gly Gln Cys Val
395 400 405 410
Asp Asp Ile Glu Ile Ile Asp Ile Asp Ile Asp Ile Ile Ile Ile Ile
410 415 420 425
Asp Asp Ile
425 430 435 440
Asp Ile Leu Ile
440 445 450 455
Asp Asp Tyr Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln
455 460 465 470
Asp Asp Tyr Leu Cys Leu Pro Asn Val Val Gly Pro Lys Cys Asp Gln
470 475 480 485

Met Lys Arg Thr Val Tyr Phe Cys Arg Glu Gly Phe Asp Gly Leu Met Tyr Ser
515 516
Arg Ala Ile Asn Gln Cys Pro Asp Asn Thr Tyr Gly Asp Val Ala
521 522 523
Asn Arg Tyr Asn Ala Cys Asp Cys Asp Ile Arg Gly Thr Glu Gly Ile
526 527 528 529
Lys Tyr Asp Lys Ala Ser Gly Arg Cys Leu Cys Asn Pro Gly Leu Thr
533 534 535 536
Asn Ile Asn Cys Asp Gln Cys Gln Arg Gly Tyr Cys Asn Asn Tyr Pro
539 540 541 542
Ser Tyr Val Ala Cys His Pro Cys Phe Gln Thr Tyr Asp Ala Asp Leu
546 547 548 549
Asn Ile Ile Ala Leu Arg Phe Gly Arg Leu Arg Asn Ala Thr Ala Ser
551 552 553 554 555
Leu Thr Ser Gly Pro Gly Leu Glu Asp Arg Gly Leu Ala Ser Arg Ile
559 560 561 562 563
Asp Asp Ala Lys Ser Lys Glu Gln Ile Arg Ala Val Leu Ser Ser
568 569 570 571 572 573 574 575
Ile Ala Val Thr Glu Gln Glu Val Ala Gln Val Ala Ser Ala Ile Leu
579 580 581 582 583 584 585 586
Asn Leu Asn Arg Thr Leu Gln Gly Leu Gln Leu Asp Leu Pro Leu Glu
589 590 591 592 593 594 595 596
Asn Ile Thr Leu Ser Leu Pro Arg Asp Leu Glu Ser Leu Asp Arg Ser
601 602 603 604 605 606 607 608
Ile Asn Gly Leu Leu Thr Met Tyr Gln Arg Lys Arg Glu Gln Phe Glu
615 616 617 618 619 620 621 622
Asp Ile Ser Ser Ala Asp Pro Ser Gly Ala Phe Arg Met Leu Ser Thr
629 630 631 632 633 634 635 636
Asn Tyr Glu Gln Ser Ala Gln Ala Gln Gln Val Ser Asp Ser Ser
645 646 647 648 649 650 651 652
Asn Leu Leu Asp Gln Leu Arg Asp Ser Arg Arg Glu Ala Glu Arg Leu
659 660 661 662 663 664 665 666
Val Asn Ile Ala Gly Gly Gly Gly Thr Gly Ser Pro Lys Leu Val
675 676 677 678 679 680 681 682
Asn Leu Asn Leu Glu Met Ser Ser Leu Pro Asp Leu Thr Pro Thr Phe
695 696 697 698 699 700 701 702
Asn Asp Leu Cys Gly Asn Ser Arg Gln Met Ala Cys Thr Pro Ile Ser
715 716 717 718 719 720 721 722
Asn Asp Leu Cys Ile Asp Asp Asn Asp Thr Ala Ile Ile Asp
729 730 731 732 733 734 735 736
Asn Asp Asp Ile Val Leu Ile Asn Ala Ile Ile Ala Phe Leu Met Ala
749 750 751 752 753 754 755 756
Asn Ile Ala Glu Gln Leu Arg Gly Phe Asn Ala Gln Leu Gln Asn
769 770 771 772 773 774 775 776
Asn Asp Ile Met Ile Asn Ala Ala Glu Gln Ser Ala Ser Gln Ile Gln
789 790 791 792 793 794 795 796
Asn Asp Asp Ile Asn Leu Ile Thr Gln Val Asp Ala Leu Asn Asp Ile

Val Ile Ile Ile Thr Asp Ile Asp Thr Asp Ala Ala Thr Ile Gln Gln Val
 905 910
 Val Ile Ala Ala Leu Ala Leu Trp Leu Ile Thr Asp Ser Ala Thr Val
 915 920 925
 Ile Ile Asp Met Asn Glu Ile Gln Ala Ile Ala Arg Leu Ile Asp
 930 935 940
 Ile Ile Ile Ile Leu Ser Gln Thr Lys Gln Asp Ile Ala Arg Ala Arg
 945 950 955 960
 Ile Ile Ile Ala Glu Ala Glu Gln Ala Arg Ser Arg Ala His Ala Val
 965 970 975 980
 Ile Asp Gln Val Glu Asp Val Val Gly Asn Leu Arg Gln Gly Thr Val
 985 990
 Ala Leu Gln Glu Ala Gln Asp Thr Met Gln Gly Thr Ser Arg Ser Leu
 995 1000 1005
 Arg Leu Ile Gln Asp Arg Val Ala Glu Val Gln Gln Val Leu Arg Pro
 1010 1015 1020
 Ala Gln Lys Leu Val Thr Ser Met Thr Lys Gln Leu Gly Asp Phe Trp
 1025 1030 1035 1040
 Thr Asp Met Gln Glu Leu Arg His Gln Ala Arg Gln Gln Gly Ala Glu
 1045 1050 1055
 Ala Val Gln Ala Gln Gln Leu Ala Glu Gly Ala Ser Glu Gln Ala Leu
 1060 1065 1070
 Ser Ala Gln Glu Gly Phe Glu Arg Ile Lys Gln Lys Tyr Ala Glu Leu
 1075 1080 1085
 Asp Asp Arg Leu Gly Gln Ser Ser Met Leu Gly Glu Gln Gly Ala Arg
 1090 1095 1100
 Ile Gln Ser Val Lys Thr Glu Ala Glu Leu Phe Gly Glu Thr Met
 1105 1110 1115 1120
 Ile Met Met Asp Arg Met Lys Asp Met Glu Leu Glu Leu Leu Arg Gly
 1125 1130 1135
 Asp Gln Ala Ile Met Leu Arg Ser Ala Asp Leu Thr Gly Leu Glu Lys
 1140 1145 1150
 Asp Val Gln Ile Arg Asp His Ile Asn Gly Arg Val Leu Tyr Tyr
 1155 1160 1165
 Ile Thr Tyr Lys
 1170

Val Ile Ile Ile Leu Leu Val Phe Leu Leu Leu Leu Ile Gly Ser Tyr
 1175 1180 1185 1190 1195 1200
 Ile Ile Ile Tyr Asn Ile Phe Tyr Tyr Tyr Ile Arg Ser Ala Asn Asp

... Val Thr Ile Glu Glu Thr Leu Phe Thr Arg Ile Leu Thr
 105 110 115 120
 ... Asp Ile Ile Ser Leu Gly Ile Glu Ala Leu Ala Ser Ile Thr Arg
 125 130 135 140 145
 ... Ala Ala Tyr Thr Val Ile Thr Ala Thr Ala Ser Thr Arg Thr Thr
 150 155 160 165 170
 ... Ile Ile Ile Leu Pro His Ser Leu Thr Gly Cys Val Ile Ile Glu Trp
 175 180 185 190 195
 ... Val Thr Ile Cys Gly Leu Glu Pro Phe
 200 205 210

1977
H. M. Capions

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III. Applications

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二

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Homo sapiens

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 RNA
 Human Sapiens

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 11 tttttttttt ccaadccggagg gtggaaacggc gtcggcgccga gcttgtgggc cgcgtgttc 60
 12 aatggggaa tggcgctgag gccggccggag ggggtgtccg agccccacgac cgtggcgttt 120
 13 ttttttttt ccggccgggt cgtgcattcc ttctccata acgtgggccc gggggacaaaa 180
 14 atttttttt ttttccactta cggctatcaa ggagggacca atgagcaatg gcagatgagt 240
 15 tttttttttt tttttttttt ccggccgggtt acctgcacca tctggaggcc ccaggggaag 300
 16 tttttttttt tttttttttt gttcaaggca gaggtgggg gggctgagat tgagtacgcc 360
 17 tttttttttt tttttttttt attgaaacggc attgaaagg gaaagtgtatq tccctctgaa aactgagdaa 420
 18 tttttttttt tttttttttt cttttttttt agtggctcac agggccgggg cattcaaago tggatgtgtcc 480
 19 tttttttttt tttttttttt ggcatacgcc actgagctq 519

1. *Homo sapiens*

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ttttttttttt	tgtctactgg	cccatattgttc	ctgtctgcgg	gctcctacgg	actgcccttc	60
ttttttttttt	tataactactc	aaacagcgcc	aaacgaccaga	accttaggca	caatcatatgc	120
ttttttttttt	ttaatggagt	gaaggtggtg	gtggagacac	ccgaggagac	cctgttttacc	180
ttttttttttt	ctgtggggcc	ccagagctg	gggtccgaag	ctttggcttc	cccgaccgc	240
ttttttttttt	gtacgggtgtt	tactgctacc	gccagcacta	ggacctgggg	ccctccccctg	300
ttttttttttt	tcactgactg	tytattttat	gagtgtttcg	ttttcccttg	tgggttggag	360
						366

1. H. R. sapiens

Sequence	Start	End	Length
Met Ile Leu Val Ile Ala Thr Ala Ile Ala Ala Ala Leu Ala Val Ile Leu Ile Ala Thr Ala Leu	1	10	10
Tyr Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro Cys	10	25	15
Ile Ile Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys Glu	25	40	15
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	40	55	15
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	55	60	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	60	65	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	65	70	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	70	75	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	75	80	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	80	85	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	85	90	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	90	95	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	95	100	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	100	105	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	105	110	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	110	115	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	115	120	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	120	125	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	125	130	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	130	135	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	135	140	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	140	145	5
Ile Ile Ala Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val His Ara	145	150	5

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H. H. Happelius

$$\dots \cdot (11) \dots (1001)$$

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tttccccggg cacggcattcc tgtgtctgtgg gggctacgag gaaagatcta attatc atg 59
Met

Met

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...ttt ttt ttt ttt cag ttt ctt atg tgc ctg tcc ctg tgc aca gcc ttt gcc
Leu Leu Arg Gln Phe Leu Met Cys Leu Ser Leu Cys Thr Ala Phe Ala
5 10 15

...atcatatccaaacaa gaa aag aag gac cgt gta cat cat gag cct cag 155
Leu Thr Lys Pro Thr Glu Lys Lys Asp Arg Val His His Glu Pro Gln
20 25 30

...attattaaatcatatgatgtcagagttttatggatcat 23
Ile Ile Asp Lys Val His Asn Asp Ala Gln Ser Phe Asp Tyr Asp His
49 45

the first and the last one did not fit the other two. The first pair Lys-Glu and Leu-Gly-Lys the tail of the Lys-Asp

111
Lam Yen Mai Anh His Asp Glu Phe

17

H. m. sapiens

• main feature

and λ , T, C or G

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atgttttttttata gtnccgacgt cgtgggtgtt tggtgtgagg ctgcgagccg ccgcggccac 60
tttttttttttac acggtcgcct gccacaggtg tctgcaattg aactccaagg tgcaaga atg 119
Met

...ttt ttt taa gta gct gta ttc ctc agt gtg gcc ctg ggc att ggt gcc 167
 Tyr Tyr Lys Val Ala Val Phe Leu Ser Val Ala Leu Gly Ile Gly Ala
 5 10 15

... Val Val Ile Asp Asp Phe Glu Asp Gly Gly Lys His Trp Val Val Ile
 25 30

As the HEP and ASK 8211-111 Asp 8211-111

140 Val Ala Leu Leu Leu Ile Asp Ala Val Ala Leu Arg Ile Ala Glu
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 142 Met Thr Ile Ile Thr Thr Val Ala Ile Asp Val Arg Ile Gly Gly
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the first time in the history of the world, the people of the United States have been called upon to decide whether they will submit to the law of force, and let a一小部分 of their country be held at bay by a一小部分 of their neighbors, or whether they will, as a nation, assert and maintain the right which every nation has of self-government and self-preservation.

and that the legislature will immediately accredit the constitution of the state of Oregon.

Met Gly Val Lys Leu

...atggatcataatctacactttccatgtgtatgttttc 164
 ...IleIleArgMetIleIleTyrLeuThrPheProValAlaMetPhe
 ...
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 15
 16

... GAG TTT GAG GCA GAG TGG TTT GAA GAC GAT ATC ATA CAA CGT 212
 Ser Thr Arg Asn Glu Ala Glu Trp Phe Glu Asp Asp Val Ile Gln Arg
 25 30 35

... att gat ctg tgg cca cct gag aag ctt caa gag ata gag gaa ttc 260
Arg Arg Glu Leu Trp Pro Pro Glu Lys Leu Gln Glu Ile Glu Glu Phe
45 50

...ttt tta cggtt aag cgg cgg gag gag aag ctc ctt cgc gag gcc 308
 Tyr His Arg Leu Arg Lys Arg Glu Glu Lys Leu Leu Arg Asp Ala
 60 65

catatgtttatcc tgaggcctcc aagtgggaaqt cctagccccat cccctgatga
Met. His. Asn. Ser.

actttttt tactcaggcc ttgttttttc 390

Met Am Pro The The Leu Leu

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Arg Ser Cys Gln Gln Ala His Leu Pro Gly Leu Leu His Ala Gln Gln Ala Cys Ser Arg
 15 20

...ttt ttt tat cca cct gtt ggg gac ctg ctt att ggg ayy acc cgg 570
Tyr Ala Tyr Pro Pro Val Gly Asp Leu Leu Val Gly Arg Thr Arg
30 35

...ttt cta tct tca tct acc tgt gga ctg acc aag cct gag acc tac 918
Ile Ileu Arg Ala Ser Ser Thr Cys Gly Leu Thr Lys Pro Glu Thr Tyr
45 50 55

* * * cat tat ggc gag tgg cag atg aaa tgc tgc aag tgt gac tcc 966
 * * * Tyr Tyr Gly Glu Trp Gln Met Lys Cys Cys Lys Cys Asp Ser
 60 65 70

...ttatattt tac aac tac tac agt cac cga gta gag aat gtg gct tca 1014
 Asn Thr His Asn Tyr Tyr Ser His Arg Val Glu Asn Val Ala Ser
 75 80 85

... gtt tcc atg cgc tgg tgg cag tcc cag aat gat gtg aac cct 1062
 Val Ser Gly Pro Met Arg Trp Trp Gln Ser Gln Asn Asp Val Asn Pro
 9 35 100

ctt ttt ttg ctg gac ctg gac agg aga ttc cag ctt caa gaa gtc l110
Leu Ile Val Leu Asp Leu Asp Arg Arg Phe Gln Leu Gln Glu Val

and the rest of it and was trying to get the other part of the last
one off by the side line. The top front tail fin was torn all the

ttt ccc ttg ttt tac gag tac att cat acc gat gat Gln Val
 Ile Ser Arg Val Asn Lys Glu Ser Leu Ile Glu Arg Ile Asn Ala Arg
 175 180

ttt ccc ttg ttt gag gtc caa ctt aac ctt att dat tta gtg tet ptt
 Ile Arg Ile Ily Lys Val Gln Leu Asn Leu Met Asp Leu Val Ser Gly
 190 195

ctt ctt ttt att ctt aat ctt ctt aat ctt ctt aat ctt aat ctt aat ctt
 Ala Thr Gln Ser Gln Lys Ile Gln Glu Val Gly Glu Ile Thr
 205 210

ctt ctt ttt att aat ttc acc agg ctg gcc ctt gtg ccc ctt aag ggc
 Asn Leu Asn Val Asn Phe Thr Arg Leu Ala Pro Val Pro Gln Arg Gly
 220 225 230

ctt ctt ttt att aat agc gcc tac tat gct gtg ttt cag ctc cgt ctg ctt
 Ile Asn Ile Ily Ser Ala Tyr Tyr Ala Val Ser Gln Leu Arg Leu Gln
 240 245

ctt ctt ttt att ttt ttt ctt
 Gly Ser Tyr Phe Cys His Gly His Ala Asp Arg Cys Ala Pro Lys Pro
 255 260

ctt aac ctt ttt gca ggc ccc tcc acc gct gtg cag gtc cac gat gtc ttt
 Ily Ala Ser Ala Gly Pro Ser Thr Ala Val Gln Val His Asp Val Cys
 270 275

ctt ctt ttt ctt
 Val Tyr Gln His Asn Thr Ala Gly Pro Asn Cys Glu Arg Cys Ala Pro
 285 290 295

ctt ctt ttt ctt
 Ile Tyr Asn Asn Asn Pro Trp Arg Pro Ala Glu Gln Asp Ala His
 305 310

ctt ctt ttt ctt
 Ile Asn Ile Ily Asp Ile Asn Ily His Ile Ile Thr Ily His Ile
 315 320

ctt ctt ttt ctt
 Ile Asn Ile Ily Asp Ile Asn Ily His Ile Ile Thr Ily His Ile
 325 330

THE FRENCH REVOLUTION AND THE END OF THE 18TH CENTURY

Human Nature

... (E03)

ATGAAATGCTTGAGCTGCTGTTGGGGACG	GGCCCCAGCC	TGGCCCGGGT	120
ATGAGAGATGATGAGATGATGATGATGATG	ATGATGATGATGATGATGATGATGATGATG	ATGATGATGATGATGATGATGATGATGATG	170
Met Gly Leu Leu Leu Leu Val Pro Leu Leu			
1	5	10	

... tcc tcc gga tcc tac gga ctg ccc ttc tac aac ggc ttc tac tac tcc 218
 Leu Pro Gly Ser Tyr Gly Leu Pro Phe Tyr Asn Gly Phe Tyr Tyr Ser
 15 20 25

... ttt ttt tcc aac gac cag aac cta ggc aac ggt cat ggc aaa gac ctc 266
 Tyr Tyr Ala Asn Asp Gln Asn Leu Gly Asn Gly His Gly Lys Asp Leu
 ...
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... -cys-ala-tyr-ala-cys-tyr-glyc-ala-alu-glyc-acu-cys-thr ... 314
... -Cys-Ala-Tyr-Ala-Lys-Leu-Val-Val-Glu-Thr-Pro-Glu-Glu-Thr-Leu-Phe
... -Cys-Ala-Tyr-Ala-Lys-Leu-Val-Val-Glu-Thr-Pro-Glu-Glu-Thr-Leu-Phe

Leu Ile Ile Trp Ile Val Ile Phe Tyr Cys Gly Leu Glu Ile Phe
111 120

Humanus
Homo sapiens

... 740 . . . (597)

...tac act ctg gcc aga gat acc aca gtc aaa cct gaa gcc 159
 ...Ser Tyr Thr Leu Ala Arg Asp Thr Thr Val Lys Pro Gly Ala
 ...
 20 25

...cgt ttt aca aag gag tat cya ccc aaa cty ccc tag acc ctc tcc 207
 ...t, Lys Asp Ile Arg Pro Lys Leu Pro Gln Thr Leu Ser

Thy Name Thy Name Thy Name Thy Name Thy Name Thy Name Thy Name

